

## RAW SEQUENCE LISTING

EF5

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/649,413A  
Source: 1FW16  
Date Processed by STIC: 4/4/07

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IFW16

## RAW SEQUENCE LISTING

DATE: 04/04/2007

PATENT APPLICATION: US/10/649,413A

TIME: 14:56:24

Input Set : N:\efs\04\_04\_07\10649413A\_efs\224160\_ST25\_2.txt

Output Set: N:\CRF4\04042007\J649413A.raw

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4 <110> APPLICANT: Ullrich, Axel
5      Bange, Johannes
6      Knyazev, Pjotr
8 <120> TITLE OF INVENTION: Use of inhibitors for the treatment of RTK-hyperfunction-
induced
9      disorders, particularly cancer
11 <130> FILE REFERENCE: 205884
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/649,413A
C--> 14 <141> CURRENT FILING DATE: 2003-08-27
16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/00405
17 <151> PRIOR FILING DATE: 1999-01-22
19 <150> PRIOR APPLICATION NUMBER: DE 198 02 377.4
20 <151> PRIOR FILING DATE: 1998-01-22
22 <160> NUMBER OF SEQ ID NOS: 9
24 <170> SOFTWARE: PatentIn Ver. 3.4
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 25
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: DOMAIN
33 <222> LOCATION: (1)..(25)
34 <223> OTHER INFORMATION: amino acid sequence of
35      FGFR-4 (mutant) between positions 366-390
37 <400> SEQUENCE: 1
38 Arg Tyr Thr Asp Ile Ile Leu Tyr Ala Ser Gly Ser Leu Ala Leu Ala
39 1          5          10          15
41 Val Leu Leu Leu Leu Ala Arg Leu Tyr
42      20          25
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45 <211> LENGTH: 25
46 <212> TYPE: PRT
47 <213> ORGANISM: Homo sapiens
49 <220> FEATURE:
50 <221> NAME/KEY: DOMAIN
51 <222> LOCATION: (1)..(25)
52 <223> OTHER INFORMATION: amino acid sequence of
53      FGFR-4 (wild-type) between positions 366-390
55 <400> SEQUENCE: 2
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57 1          5          10          15
59 Val Leu Leu Leu Leu Ala Gly Leu Tyr
60      20          25
62 <210> SEQ ID NO: 3

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63 <211> LENGTH: 29  
64 <212> TYPE: DNA  
65 <213> ORGANISM: artificial sequence  
67 <220> FEATURE:  
68 <223> OTHER INFORMATION: PCR primer for the amplification of FGFR-4 (wild-type and mutant)  
70 <400> SEQUENCE: 3  
71 gctcagaggg cgggcggggg tgccggccg 29  
73 <210> SEQ ID NO: 4  
74 <211> LENGTH: 33  
75 <212> TYPE: DNA  
76 <213> ORGANISM: artificial sequence  
78 <220> FEATURE:  
79 <223> OTHER INFORMATION: PCR primer for the amplification of FGFR-4 (wild-type and mutant)  
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84 <210> SEQ ID NO: 5  
85 <211> LENGTH: 24  
86 <212> TYPE: DNA  
87 <213> ORGANISM: artificial sequence  
89 <220> FEATURE:  
90 <223> OTHER INFORMATION: PCR primer for the amplification of the transmembrane domain of FGFR-4  
91 (wild-type and mutant)  
93 <400> SEQUENCE: 5  
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96 <210> SEQ ID NO: 6  
97 <211> LENGTH: 23  
98 <212> TYPE: DNA  
99 <213> ORGANISM: artificial sequence  
101 <220> FEATURE:  
102 <223> OTHER INFORMATION: PCR primer for the amplification of the transmembrane domain of FGFR-4  
103 (wild-type and mutant)  
105 <400> SEQUENCE: 6  
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110 <212> TYPE: DNA  
111 <213> ORGANISM: artificial sequence  
113 <220> FEATURE:  
114 <223> OTHER INFORMATION: primer for sequencing of the transmembrane domain of FGFR-4  
115 (wild-type and mutant)  
117 <400> SEQUENCE: 7  
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120 <210> SEQ ID NO: 8  
121 <211> LENGTH: 25  
122 <212> TYPE: DNA  
123 <213> ORGANISM: artificial sequence  
125 <220> FEATURE:  
126 <223> OTHER INFORMATION: primer for sequencing of the transmembrane domain of FGFR-4  
127 (wild-type and mutant)

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135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 9
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144 Pro Pro Val Leu Ser Leu Glu Ala Ser Glu Glu Val Glu Leu Glu Pro
145 20 25 30
148 Cys Leu Ala Pro Ser Leu Glu Gln Gln Glu Gln Glu Leu Thr Val Ala
149 35 40 45
152 Leu Gly Gln Pro Val Arg Leu Cys Cys Gly Arg Ala Glu Arg Gly Gly
153 50 55 60
156 His Trp Tyr Lys Glu Gly Ser Arg Leu Ala Pro Ala Gly Arg Val Arg
157 65 70 75 80
160 Gly Trp Arg Gly Arg Leu Glu Ile Ala Ser Phe Leu Pro Glu Asp Ala
161 85 90 95
164 Gly Arg Tyr Leu Cys Leu Ala Arg Gly Ser Met Ile Val Leu Gln Asn
165 100 105 110
168 Leu Thr Leu Ile Thr Gly Asp Ser Leu Thr Ser Ser Asn Asp Asp Glu
169 115 120 125
172 Asp Pro Lys Ser His Arg Asp Pro Ser Asn Arg His Ser Tyr Pro Gln
173 130 135 140
176 Gln Ala Pro Tyr Trp Thr His Pro Gln Arg Met Glu Lys Lys Leu His
177 145 150 155 160
180 Ala Val Pro Ala Gly Asn Thr Val Lys Phe Arg Cys Pro Ala Ala Gly
181 165 170 175
184 Asn Pro Thr Pro Thr Ile Arg Trp Leu Lys Asp Gly Gln Ala Phe His
185 180 185 190
188 Gly Glu Asn Arg Ile Gly Gly Ile Arg Leu Arg His Gln His Trp Ser
189 195 200 205
192 Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly Thr Tyr Thr Cys
193 210 215 220
196 Leu Val Glu Asn Ala Val Gly Ser Ile Arg Tyr Asn Tyr Leu Leu Asp
197 225 230 235 240
200 Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro
201 245 250 255
204 Ala Asn Thr Thr Ala Val Val Gly Ser Asp Val Glu Leu Leu Cys Lys
205 260 265 270
208 Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu Lys His Ile Val
209 275 280 285
212 Ile Asn Gly Ser Ser Phe Gly Ala Val Gly Phe Pro Tyr Val Gln Val
213 290 295 300
216 Leu Lys Thr Ala Asp Ile Asn Ser Ser Glu Val Glu Val Leu Tyr Leu
217 305 310 315 320
220 Arg Asn Val Ser Ala Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly
221 325 330 335

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224 Asn Ser Ile Gly Leu Ser Tyr Gln Ser Ala Trp Leu Thr Val Leu Pro
225          340          345          350
228 Glu Glu Asp Pro Thr Trp Thr Ala Ala Ala Pro Glu Ala Arg Tyr Thr
229          355          360          365
232 Asp Ile Ile Leu Tyr Ala Ser Gly Ser Leu Ala Leu Ala Val Leu Leu
233          370          375          380
236 Leu Leu Ala Gly Leu Tyr Arg Gly Gln Ala Leu His Gly Arg His Pro
237 385          390          395          400
240 Arg Pro Pro Ala Thr Val Gln Lys Leu Ser Arg Phe Pro Leu Ala Arg
241          405          410          415
244 Gln Phe Ser Leu Glu Ser Gly Ser Ser Gly Lys Ser Ser Ser Ser Leu
245          420          425          430
248 Val Arg Gly Val Arg Leu Ser Ser Ser Gly Pro Ala Leu Leu Ala Gly
249          435          440          445
252 Leu Val Ser Leu Asp Leu Pro Leu Asp Pro Leu Trp Glu Phe Pro Arg
253          450          455          460
256 Asp Arg Leu Val Leu Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln
257 465          470          475          480
260 Val Val Arg Ala Glu Ala Phe Gly Met Asp Pro Ala Arg Pro Asp Gln
261          485          490          495
264 Ala Ser Thr Val Ala Val Lys Met Leu Lys Asp Asn Ala Ser Asp Lys
265          500          505          510
268 Asp Leu Ala Asp Leu Val Ser Glu Met Glu Val Met Lys Leu Ile Gly
269          515          520          525
272 Arg His Lys Asn Ile Ile Asn Leu Leu Gly Val Cys Thr Gln Glu Gly
273          530          535          540
276 Pro Leu Tyr Val Ile Val Glu Cys Ala Ala Lys Gly Asn Leu Arg Glu
277 545          550          555          560
280 Phe Leu Arg Ala Arg Arg Pro Pro Gly Pro Asp Leu Ser Pro Asp Gly
281          565          570          575
284 Pro Arg Ser Ser Glu Gly Pro Leu Ser Phe Pro Val Leu Val Ser Cys
285          580          585          590
288 Ala Tyr Gln Val Ala Arg Gly Met Gln Tyr Leu Glu Ser Arg Lys Cys
289          595          600          605
292 Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Thr Glu Asp Asn
293          610          615          620
296 Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg Gly Val His His Ile
297 625          630          635          640
300 Asp Tyr Tyr Lys Lys Thr Ser Asn Gly Arg Leu Pro Val Lys Trp Met
301          645          650          655
304 Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr His Gln Ser Asp Val
305          660          665          670
308 Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Phe Thr Leu Gly Gly Ser
309          675          680          685
312 Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe Ser Leu Leu Arg Glu
313          690          695          700
316 Gly His Arg Met Asp Arg Pro Pro His Cys Pro Pro Glu Leu Tyr Gly
317 705          710          715          720
320 Leu Met Arg Glu Cys Trp His Ala Ala Pro Ser Gln Arg Pro Thr Phe

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321					725					730					735	
324	Lys	Gln	Leu	Val	Glu	Ala	Leu	Asp	Lys	Val	Leu	Leu	Ala	Val	Ser	Glu
325					740					745					750	
328	Glu	Tyr	Leu	Asp	Leu	Arg	Leu	Thr	Phe	Gly	Pro	Tyr	Ser	Pro	Ser	Gly
329					755					760					765	
332	Gly	Asp	Ala	Ser	Ser	Thr	Cys	Ser	Ser	Ser	Asp	Ser	Val	Phe	Ser	His
333					770					775					780	
336	Asp	Pro	Leu	Pro	Leu	Gly	Ser	Ser	Ser	Phe	Pro	Phe	Gly	Ser	Gly	Val
337	785									790					795	800
340	Gln	Thr														

**VERIFICATION SUMMARY**

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Input Set : N:\efs\04\_04\_07\10649413A\_efs\224160\_ST25\_2.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date